WHAT IS CLAIMED IS:

1. A method for the identification and isolation of a genetic sequence from an organism, wherein disruption of genomic DNA of said organism by a transposable element flanking said genetic sequence is associated with a mutant phenotype, said method comprising the following steps:

a) segregating a plurality of organisms by the presence or absence of said mutant phenotype, wherein the genomic DNA of each organism comprises at least one copy of said transposable element;

b) obtaining a mutant genomic DNA sample from at least one of said organisms exhibiting said mutant phenotype and a wild-type genomic DNA sample from at least one of said organisms not exhibiting said mutant phenotype;

c) fragmenting at least one of said mutant and at least one of said wild-type genomic DNA samples to produce DNA fragments;

d) attaching an adapter to at least one of said mutant DNA fragments and to at least one of said wild-type DNA fragments, resulting in a collection of adapter-modified DNA fragments;

e) amplifying said mutant and wild-type adapter-modified DNA fragments to yield amplification products comprising said genetic sequence flanked by: 1) a transposable element derived sequence and, 2) an adapter derived sequence, wherein said amplification employs at least two oligonucleotide primers, with one of said primer sequences selectively hybridizing, under stringent hybridization conditions, to said adapter sequence and the other primer selectively hybridizing, under stringent hybridization conditions, to said transposable element; and

f) isolating an amplification product present in said organism exhibiting said mutant phenotype and absent in said organism not exhibiting said mutant phenotype, wherein said isolated amplification product comprises said genetic sequence associated

with said mutant phenotype.

2. The method of claim 1, wherein step (f) comprises using cosegregation analysis to isolate an amplification product that cosegregates with said mutant phenotype.

3. The method of claim 1, wherein step (f) comprises using bulked segregant analysis to isolate said amplification product.

4. The method of claim 1, wherein said transposable element is a transposable element that comprises a terminal inverted repeat (TIR) sequence.

5. The method of claim 4, wherein said transposable element is a member of the *Mutator* family of transposable elements.

6. The method of claim 5, wherein said primer is a *Mutator*-TIR primer derived from said TIR sequence.

7. The method of claim 1, wherein said organisms are plants.

8. The method of claim 7, wherein said plant is a maize plant.

9. The method of claim 1, further comprising a second amplification to preferentially amplify adapter-modified DNA fragments, wherein said preliminary amplification employs at least two oligonucleotide primers, with one of said primers selectively hybridizing, under stringent hybridization conditions, to said adapter sequence and the other primer selectively hybridizing, under stringent hybridization conditions, to said insertion sequence.

10. The method of claim 9, wherein said primers are nested with the primers of claim 1.

11. The method of claim 1, wherein said amplification is achieved by polymerase chain reaction (PCR).

12. The method of claim 1, wherein the fragmentation of step (c) is achieved by digestion with at least one restriction enzyme.

13. The method of claim 1, wherein said first genomic DNA sample of step (b) comprises genomic DNA from at least 2 organisms and said second genomic DNA sample comprises genomic DNA of 10 organisms.

14. The method of claim 1, wherein at least one of said primers is labeled.

15. A method for identifying one or more locations of a genomic insertion by a transgene in genomic DNA of an organism, said method comprising the following steps:

a) isolating a genomic DNA sample from said organism;

b) fragmenting said isolated genomic DNA sample, said fragmentation resulting in a DNA sample that comprises a collection of DNA fragments;

c) attaching an adapter sequence to at least one of said DNA fragments, said attachment resulting in a DNA sample that comprises a collection of adapter-modified DNA fragments;

d) amplifying said adapter-modified DNA fragments to yield an amplification product comprising said genomic insertion-derived sequence flanked by: 1) a transgene-derived sequence and, 2) an adapter-derived sequence, wherein said amplification employs at least two oligonucleotide primers, with one of said primer sequences selectively hybridizing, under stringent hybridization conditions, to said adapter sequence and the other primer sequence selectively hybridizing, under stringent hybridization conditions, to said transgene-derived sequence; and

e) analyzing said amplification products to identify said inserted locations of said transgene.

16. The method of claim 15, wherein said organism is a plant.

17. The method of claim 15, further comprising a second amplification to preferentially amplify adapter-modified DNA fragments, wherein said preliminary amplification employs at least two oligonucleotide primers, with one of said primers selectively hybridizing, under stringent hybridization conditions, to said adapter sequence and the other primer selectively hybridizing, under stringent hybridization conditions, to said transgene.

~~16~~ 18. The method of claim ~~16~~, wherein said transgenic organism is a maize plant.

~~18~~ 19. The method of claim ~~17~~, wherein said primers are nested with the primers of claim 15.

~~19~~ 20. The method of claim 15, wherein said amplification is achieved by polymerase chain reaction (PCR).

~~20~~ 21. The method of claim 15, wherein the fragmentation of step (b) is achieved by digestion with at least one restriction enzyme.